

Figure 1a**Variable Heavy Chain DNA****3077_VH1B (SEQ ID NO: 1):**

(1) CAGGTGCAAT TGGTCAGAG CGGCGCGGAA GTGAAAAAAC CGGGCGCGAG
 (51) CGTAAAGTG AGCTGCAAAG CCTCCGGATA TACCTTTACT TCTTATTCTA
 (101) TTAATTGGGT CCGCCAAGCC CCTGGCAGG GTCTCGAGTG GATGGGCTAT
 (151) ATCGATCCGA ATCGTGCAGA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
 (201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAACGTGA
 (251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
 (301) ATTTATTTA TTCAATGGTAT GCTTGATTT TGGGGCAAG GCACCCTGGT
 (351) GACGGTTAGC TCA

3079_VH3 (SEQ ID NO: 2):

(1) CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
 (51) CCTGCGTCTG AGCTGCGCG CTTCCGGATT TACCTTTCT AATTATGGTA
 (101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
 (151) ATCCGTTCTG ATGGTAGCTG GACCTATTAT GCGGATAGCG TGAAAGGCCG
 (201) TTTTACCAATT TCACGTGATA ATTGAAAGA CACCGCTGTAT CTGCAAATGA
 (251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTCGTTAT
 (301) TGGTCTAAGT CTCATGCTTC TGTTACTGAT TATTGGGCC AAGGCACCC
 (351) GGTGACGGTT AGCTCA

3080_VH3 (SEQ ID NO: 3):

(1) CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
 (51) CCTGCGTCTG AGCTGCGCG CTTCCGGATT TACCTTTCT TCTTATGGTA
 (101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
 (151) ATCTATTCTG ATGGTAGCAA TACCTTTAT GCGGATAGCG TGAAAGGCCG
 (201) TTTTACCAATT TCACGTGATA ATTGAAAGA CACCGCTGTAT CTGCAAATGA
 (251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTAATATG
 (301) TATCGTTGGC CTTTCATTA TTTTTTGAT TATTGGGCC AAGGCACCC
 (351) GGTGACGGTT AGCTCA

3100_VH3 (SEQ ID NO: 4):

(1) CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
 (51) CCTGCGTCTG AGCTGCGCG CTTCCGGATT TACCTTTCT TCTAATGGTA
 (101) TGTCTTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
 (151) ATCTCTTATC TTTCTAGCTC TACCTATTAT GCGGATAGCG TGAAAGGCCG
 (201) TTTTACCAATT TCACGTGATA ATTGAAAGA CACCGCTGTAT CTGCAAATGA
 (251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTTTAT
 (301) GGTTATTTA ATTATGCTGA TGTTGGGCC CAAGGCACCC TGGTGACGGT
 (351) TAGCTCA

3077_1_VH1B (SEQ ID NO: 31):

(1) CAGGTGCAAT TAGTCCAAAG TGGTGCAGAG GTGAAAAAAC CGGGCGCGAG
 (51) CGTAAAGTG AGCTGCAAAG CCTCCGGATA TACCTTTACT TCTTATTCTA

(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAACTGA
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
(301) ATTTATTTA TTCATGGTAT GCTTGATTT TGGGGCCAAG GCACCCTGGT
(351) GACGGTTAGC TCA

Figure 1b**Variable Heavy Chain Peptide
(CDR Regions in Bold)****3077_VH1B (SEQ ID NO: 5):**

(1) QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYSINWVRQA PGQGLEWMGY
(51) IDPNRGNTNY AQKFQGRVTM TRDTSISTAY MELSSLRSED TAVYYCAREY
(101) IYFIHGMLDF WGQGTLVTVS S

3079_VH3 (SEQ ID NO: 6):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS NYGMHWVRQA PGKGLEWVSN
(51) IRSDDGSWTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARRY
(101) WSKSHASVTD YWGQGTLVTV SS

3080_VH3 (SEQ ID NO: 7):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVSN
(51) IYSDGSNTFY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARNM
(101) YRWPFHYFFD YWGQGTLVTV SS

3100_VH 3 (SEQ ID NO: 8):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS SNGMSWVRQA PGKGLEWVSN
(51) ISYLSSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARFY
(101) GYFNYADVWG QGTLTVSS

Figure 2a**Variable Light Chain DNA****3077_Vk kappa 2 (SEQ ID NO: 9):**

(1) GATATCGTGA TGACCCAGAG CCCACTGAGC CTGCCAGTGA CTCCGGGCGA
 (51) GCCTGCGAGC ATTAGCTGCA GAAGCAGCCA AAGCCTGCTT TTTATTGATG
 (101) GCAATAATTA TCTGAATTGG TACCTTCAAA AACCAAGTCA AAGCCCCGAG
 (151) CTATTAATTTC ATCTTGGTTC TAATCGTGCC AGTGGGGTCC CGGATCGTTT
 (201) TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT AGCCGTGTGG
 (251) AAGCTGAAGA CGTGGGCGTG TATTATTGCC AGCAGTATTG TTCTAAGTCT
 (301) GCTACCTTTG GCCAGGGTAC GAAAGTTGAA ATTAAACGTA CG

3079_Vk kappa 1 (SEQ ID NO: 10):

(1) GATATCCAGA TGACCCAGAG CCCGTCTAGC CTGAGCGCGA GCGTGGGTGA
 (51) TCGTGTGACC ATTACCTGCA GAGCGAGCCA GGATATTCT GCTTTCTGA
 (101) ATTGGTACCA GCAGAAACCA GGTAAGCAC CGAAACTATT AATTATAAG
 (151) GTTTCTAATT TGCAAAGCGG GGTCCCGTCC CGTTTAGCG GCTCTGGATC
 (201) CGGCACTGAT TTTACCTGA CCATTAGCAG CCTGCAACCT GAAGACTTG
 (251) CGACTTATTAA TTGCCAGCAG GCTTATTCTG GTTCTATTAC CTTTGGCCAG
 (301) GGTACGAAAG TTGAAATTAA ACGTACG

3080_Vl lambda 3 (SEQ ID NO: 11):

(1) GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
 (51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTAATAAG TATGTTCTT
 (101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTGTTGTGAT TTATGGTGAT
 (151) AATAATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
 (201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
 (251) ATTATTATTG CTCTTCTTAT GATTCTTCTT ATTTTGTGTT TGGCGGCGGC
 (301) ACGAAGTTAA CCGTTCTTGG CCAG

3100_Vl lambda 3 (SEQ ID NO: 12):

(1) GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
 (51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTCATTAT TATGCTTCTT
 (101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTCTTGTGAT TTATCGTGAT
 (151) AATGATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
 (201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
 (251) ATTATTATTG CCAGTCTTAT GATTATCTTC ATGATTGTT GTTTGGCGGC
 (301) GGCACGAAGT TAACCCTTCT TGGCCAG

Figure 2b**Variable Light Chain Peptide**
(CDR Regions in Bold)**3077_Vk kappa 2 (SEQ ID NO: 13):**

(1) DIVMTQSPLS LPVTPGEPAS ISCRESSQSL **FIDGNNYLNW YLQKPGQSPQ**
(51) LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQYSSKS
(101) ATFGQGTKVE IKRT

3079_Vk kappa 1 (SEQ ID NO: 14):

(1) DIQMTQSPSS LSASVGDRVT ITCRASQDIS AFLNWYQQKP GKAPKLLIYK
(51) VSNLQSGVPS RFSGSGSGTD FTLTISSSLQP EDFATYYCQQ AYSGSITFGQ
(101) GTKVEIKRT

3080_Vl lambda 3 (SEQ ID NO: 15):

(1) DIELTQPPSV SVAPGQTARI SCSDGNIGNK YVSWYQQKPG QAPVVVIYGD
(51) NNRPSGIPER FSGSNSGNTA TLTISGTQAE DEADYYCSSY DSSYFVFHGG
(101) TKLTVLGQ

3100_Vl lambda 3 (SEQ ID NO: 16):

(1) DIELTQPPSV SVAPGQTARI SCSDGNIGHY YASWYQQKPG QAPVLVIYRD
(51) NDRPSGIPER FSGSNSGNTA TLTISGTQAE DEADYYCQSY DYLHDFVFHGG
(101) GTKLTIVLGQ

Figure 3**Variable Heavy Chain Consensus Sequences**
(CDR Regions in Bold)**VH1B Consensus (SEQ ID NO: 17):**

(1) QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYVMHWVRQA PGQGLEWMGW
(51) INPNSGGTNY AQKFQGRVTM TRDTSISTAY MELSSLRSED TAVYYCARWG
(101) **GDGFYAMDYW GQGTLTVSS**

VH3 Consensus (SEQ ID NO: 18):

(1) QVOLVESGGG LVQPAGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSA
(51) **ISGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARWG**
(101) **GDGFYAMDYW GQGTLTVVS S**

Figure 4**Variable Light Chain Consensus Sequences**(CDR Regions in **Bold**)**VL_λ3 Consensus (SEQ ID NO: 19):**

(1) SYELTQPPSV SVAPGQTARI SCSGDALGDK **YASWYQQKPG QAPVLVIYDD**
(51) SDRPSGIPER FSGSNNSGNTA TLTISGTQAE DEADYYCQQH YTTPPVFGGG
(101) TKLTVLG

VL_k1 Consensus (SEQ ID NO: 20):

(1) DIQMTQSPSS LSASVGDRVT ITCRASQGIS **SYLAWYQQKP GKAPKLLIYA**
(51) ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HYTTPPPTFGQ
(101) GTKVEIKR

VL_k2 Consensus (SEQ ID NO: 21):

(1) DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGNYLDW YLQKPGQSPQ
(51) LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQHYTTP
(101) PTFGQGTKVE IKR

Figure 5**Peptide Sequence of CD38**

(SEQ ID NO: 22):

1 mancefspvs gdkpccrlsr raqlclgvsi lvlilvvla vvvprwrqqw sgpgttkrfp
61 etvlarcvky teihpemrhv dcqsvwdafk gafiskhpcn iteedyqplm klgtqtvpca
121 killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc
181 snnpvsfwk tvsrrfaeaa cdvvhvmlng srskifdkns tfgsvevhnl qpekvqtlea
241 wvihgreds rdlcqdptik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei

Figure 6**Nucleotide Sequence of Chimeric OKT10**

Heavy Chain (SEQ ID NO: 23):

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caggtggaat tggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc
gatttttagta gatcctggat gaattgggtc cggcaggctc cagaaaaagg gctagaatgg
attggagaaa ttaatccaga tagcaagtacg ataaaactata cgacatctct aaaggataaaa
ttcatcatct ccagagacaa cgccaaaaat acgctgtacc tgcaaattgac caaagtgaga
tctgaggaca cagcccttta ttactgtgca agatatggta actggttcc ttattggggc
caagggactc tggtaactgt cagctcagcc tccaccaagg gtccatcggt cttccccctg
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gacaccctca tgatctcccg gacctctgag gtcacatgct tgggtggta cgtgagccac
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag
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tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg
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aacaactaca agaccacgcc tcccgtgctg gactccgacg gtccttctt cctctacagc
aagctcaccg tggacaagag caggtggcag cagggaaacg tcttctcatg ctccgtatg
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa
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Light Chain (SEQ ID NO: 24):

```
gatatcctga tgacccagtc tcaaaaaatc atgcccacat cagtggaga cagggtcagc
gtcacctgca aggccagtca aaatgtggat actaatgttag cctggtatca acagaaacca
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ggacagtctc ctaaagcact gatttactcg gcacatccacc gatacagtgg agtcccctgat
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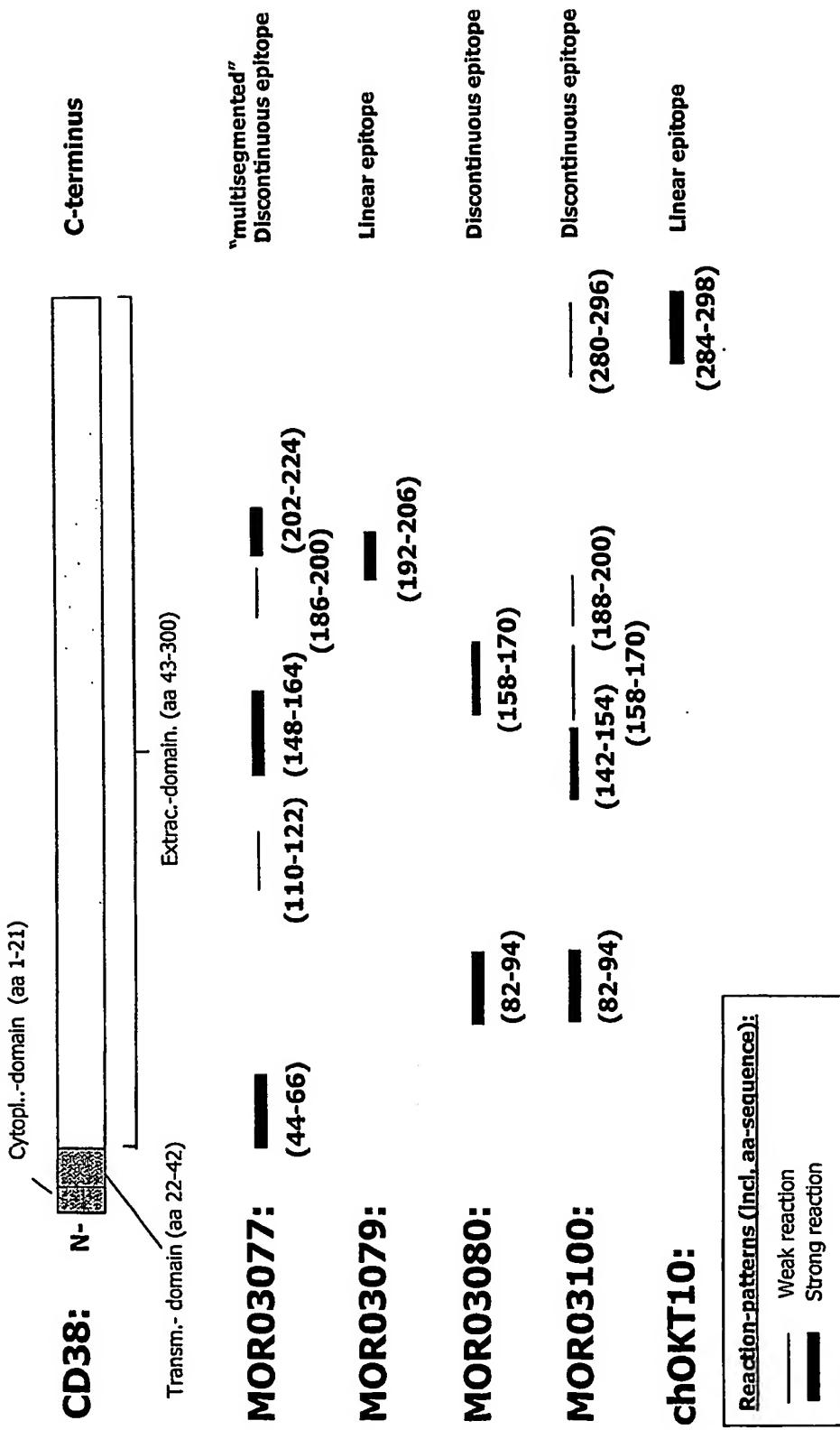
Fig.7: Schematic Overview of Epitopes

Figure 8: DNA sequence of pMOPRH®_h_IgG1_1

StyI

601 TCGCTATTAC CATGGTGTATG CGGTTTGCG AGTACATCAA TGGCGTGGAA
ACCGATAATAG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

AatII

651 TAGCGGTTTG ACTCACGGGG ATTCCAAAGT CTCCACCCCCA TTGACGTCAA
ATCGCCAAAC TGAGTCCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTCCA AAATGTCGTA
ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751 ACAACTCCGC CCCATTGACG CAAATGGCG GTAGGCGTGT ACGGTGGAG
TGTTGAGGCG GGGTAACCTGC GTTTACCCGC CATCCGCACA TGCCACCCCTC

801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTGGGT GACGAATGAC

pMOPRH®_Ig FOR 100.0%

851 GCCTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGT CGACCGATCG

M	K	H	L	W	F	F	L	L	L	V	A	A	P	R
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

901 GCCACCATGA AACACCTGTG GTTCTTCCTC CTGCTGGTGG CAGCTCCCAG
CGGTGGTACT TTGTGGACAC CAAGAAGGAG GACGACCACC GTCGAGGGTC

EcoRI

StyI

951 . W V L S Q V E F C R R L A Q
ATGGGTCTCTG TCCCAGGTGG AATTCTGCAG GCGGTTAGCT CAGCCTCCAC
TACCCAGGAC AGGGTCACC TTAAAGACGTC CGCCAATCGA GTCGAGGGTG

BpuI

951 . A S T

. W V L S Q V E F C R R L A Q

StyI

1001 . K G P S V F P L A P S S K S T S G
CAAGGGTCCA TCGGTCTTCC CCCCAGGACCC CTCCTCCAAG AGCACCTCTG
GTTCCCAGGT AGCCAGAAGG GGGACCGTGG GAGGAGGTT TCAGTGGAGAC

BbsI

1051 . G T A A L G C L V K D Y F P E P
GGGGCACAGC GGGCCTGGC TGCCTGGTCA AGGACTACTT CCCCCAACCG
CCCCGTGTGCG CCAGGACCCG ACAGGACCAAGT TCCTGATGAA GGGGCTTGGC

V T V S W N S G A L T S G V H T F

1101 GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT
CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACgtGTGGAA

P A V L Q S S G L Y S L S S V V T

1151 CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA
GGGCGACAG GATGTCAGGA GTCCGTGAGAT GAGGGAGTCG TCGCACCCT

V P S S S L G T Q T Y I C N V N

1201 CCGTGCCTC CAGCAGCTTG GGCAACCCAGA CCTACATCTG CAACGTGAAT
GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACITTA

StyI

H K P S N T K V D K K V E P K S C

1251 CACAAGCCCC GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG
GTGTTGGGT CGTTGTGGTT CCACCTGTTT CCTCAACTCG GGTTTAAAC

D K T H T C P P C P A P E L L G G

1301 TGACAAAAT CACACATGCC CACCGTGCCT AGCACCTGAA CTCCGGGGGG
ACTGTTTGAGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC

BbsI StyI

P S V F L F P P K P K D T L M I

1351 GACCGTCAGT CTTCCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC
CTGGCAGTCA GAAGGAGAAC GGGGGTTTTG GGTTCCGTG GGAGTACTAG

BbsI

S R T P E V T C V V V D V S H E D

1401 TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA
AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCAC TCGTGTCT

BbsI

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P E V K F N W Y V D G V E V H N A

1451 CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG
GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC

K T K P R E E Q Y N S T Y R V V

1501 CCAAGACAAA GCCCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC
GGTTCTGTTT CGGCGCCCTC CTCGTATGT TGTCGTGCAT GGCCCACCAAG

S V L T V L H Q D W L N G K E Y K

1551 AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA
TCGCAGGAGT GGCAGGACGT GGTCTGACC GACTTACCGT TCCTCATGTT

C K V S N K A L P A P I E K T I S

1601 GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
CACGTTCCAG AGGTTTTC GGGAGGGTCG GGGTAGCTC TTTGGTAGA

BsrGI

1651 . K A K G Q P R E P Q V Y T L P P
 CCAAAGCCAA AGGGCAGCCC CGAGAACAC AGGTGTACAC CCTGCCCA
 GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT

S R D E L T K N Q V S L T C L V K

1701 TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA
 AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAAGTT

. G F Y P S D I A V E W E S N G Q P

1751 AGGCTTCTAT CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC
 TCCGAAGATA GGGTCGCTGT AGCGGCACCT CACCCCTCTCG TTACCCGTG

1801 . E N N Y K T T P P V L D S D G S
 CGGAGAACAA CTACAAGACC ACGGCTCCCG TGCTGGACTC CGACGGCTCC
 GCCTTTGTT GATGTTCTGG TGCGGAGGGC ACGACCTGAG GCTGCCGAGG

F F L Y S K L T V D K S R W Q Q G

1851 TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT GGCAGCAGGG
 AAGAAGGAGA TGTCGTTCGA GTGGCACCTG TTCTCGTCCA CCGTCGTCCC

BbsI

NsiI

. N V F S C S V M H E A L H N H Y T

1901 GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
 CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT

SapI

PmeI

. Q K S L S L S P G K *

1951 CGCAGAAAGAG CCTCTCCCTG TCTCCGGTA AATGAGGGCC CGTTAAACC
 GCGTCTTCTC GGAGAGGGAC AGAGGCCAT TTACTCCGG GCAAATTG

2001 CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTIGTTG
 GCGACTAGTC GGAGCTGACA CGGAAGATCA ACGGTCGGTA GACAACAAAC

pMORPH_Ig_REV 100.0%

2051 CCCCTCCCCC GTGCCTTCCT TGACCCCTGGGA AGGTGCCACT CCCACTGTCC
 GGGGAGGGGG CACGGAAGGA ACTGGGACCT TCCACGGTGA GGGTGACAGG

Figure 9: DNA Sequence of Ig kappa light chain expression vector**pMORPH®_h_Igκ_1****StyI**

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601 TCGCTATTAC CATGGTGATG CGGTTTGGC AGTACATCAA TGGGCGTGG
      AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT
651 TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCCA TTGACGTCAA
      ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT
701 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTGTA
      ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT
751 ACAACTCCGC CCCATTGACG CAAATGGCG GTAGGCGTGT ACGGTGGGAG
      TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCCTC
801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
      CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTGGGT GACGAATGAC

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pMORPH®_Ig FOR 100%**NheI**

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851 GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
      CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGT CGACCGATCG

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+1      M V L Q T   Q V F   I S L L   L W I
      StyI
-----

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901 GCCACCATGG TGTTGCAGAC CCAGGTCTTC ATTTCTCTGT TGCTCTGGAT
      CGGTGGTACC ACAACGTCTG GGTCCAGAAG TAAAGAGACA ACGAGACCTA
      BbsI
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```

+1      S G A   Y G D I   V M I   K R T   V A A
      ECORV
      BsiWI
-----
```

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951 CTCTGGTGCC TACGGGGATA TCGTGATGAT TAAACGTACG GTGGCTGCAC
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```

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+1 P S V F   I F P   P S D E   Q L K   S G T
1001 CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA ATCTGGAACCT
      GTAGACAGAA GTAGAAGGGC GGTAGACTAC TCGTCAACTT TAGACCTTGA
      BbsI
-----
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+1 A S V V C L L N N F Y P R E A K V
 1051 GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT
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+1 Q W K V D N A L Q S G N S Q E S
 1101 ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG
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+1 V T E Q D S K D S T Y S L S S T L
 1151 TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCCTG
 AGTGTCTCGT CCTGTCGTTC CTGTCGTGGA TGTCGGAGTC GTCGTGGAC

+1 T L S K A D Y E K H K V Y A C E V
 BlpI

1201 ACGCTGAGCA AAGCAGACTA CGAGAAAACAC AAAGTCTACG CCTGCGAAAGT
 TGCGACTCGT TTCTGCTGAT GCTCTTGTG TTTCAGATGC GGACGCTTCA

+1 T H Q G L S S P V T K S F N R G
 1251 CACCCATCAG GGCGCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG
 GTGGGTAGTC CCGGACTCGA CGGGCAGTG TTTCTCGAAG TTGTCCCCTC

+1 E C *

PmeI	pMORPH°_Ig_REV 100%
=====	

1301 AGTGTAGGG GCCCCTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT
 TCACAATCCC CGGGCAAATT TGGGGACTA GTCGGAGCTG ACACGGAAGA

=

1351 AGTTGCCAGC CATCTGTTGT TTGCCCTCC CCCGTGCCTT CCTTGACCCT
 TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA GGAACTGGGA

Figure 10: DNA Sequence of HuCAL® Ig lambda light chain vector**pMORPH®_h_Igλ_1**

StyI

601 TCGCTATTAC CATGGTGATG CGGTTTGGC AGTACATCAA TGGGCGTGGAA
AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

651 TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCCA TTGACGTCAA
ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
ACCCTCAAAC AAAACCGTGG TTTAGTTGC CCTGAAAGGT TTTACAGCAT

751 ACAACTCCGC CCCATTGACG CAAATGGCG GTAGGCGTGT ACGGTGGGAG
TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCCTC

801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTGGGT GACGAATGAC

pM_Ig_FOR 100.0% NheI

851 GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGT CGACCGATCG

+1 M A W A L L L L T L L T Q G T
StyI

901 GCCACCATGG CCTGGGCTCT GCTGCTCCTC ACCCTCCTCA CTCAGGGCAC
CGGTGGTACC GGACCCGAGA CGACGGAGGAGT GAGTCCCGTG

+2 T V L G Q
+1 G S W A D I V M H E V
BamHI EcoRV HpaI StyI

951 AGGATCCTGG GCTGATATCG TGATGCACGA AGTTAACCGT CCTAGGTCAG
TCCTAGGACC CGACTATAGC ACTACGTGCT TCAATTGGCA GGATCCAGTC

+2 P K A A P S V T L F P P S S E E L
StyI

1001 CCCAAGGCTG CCCCCTCGGT CACTCTGTT CCAGCCCTCCT CTGAGGAGCT
GGGTTCCGAC GGGGGAGCCA GTGAGACAAG GGCGGGAGGA GACTCCTCGA

+2 Q A N K A T L V C L I S D F Y P
1051 TCAAGCCAAC AAGGCCACAC TGGTGTGTCT CATAAGTGAC TTCTACCCGG
AGTCGGTTG TTCCGGTGTG ACCACACAGA GTATTCACTG AAGATGGGCC

+2 G A V T V A W K G D S S P V K A G
 1101 GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA
 CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT

+2 V E T T T P S K Q S N N K Y A A S
 1151 GTGGAGACCA CCACACCCCTC CAAACAAAGC ACAACAAGT ACGCGGCCAG
 CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC

+2 S Y L S L T P E Q W K S H R S Y
 1201 CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAGTCCCAC AGAACGCTACA
 GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAAGGGTG TCTTCGATGT

+2 S C Q V T H E G S T V E K T V A P
 1251 GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCT
 CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

+2 T E C S *
 1301 ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
 TGTCTTACAA GTATCCCCGG GCAAATTGG GCGACTAGTC GGAGCTGACA
 pM_Ig_REV 100%
 =====

1351 GCCTTCTAGT TGCCAGCCAT CTGTTGTTG CCCCTCCCC GTGCCTTCCT
 CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
 pM_Ig_REV 100.0%
 =====

Fig. 11: Proliferation Assay

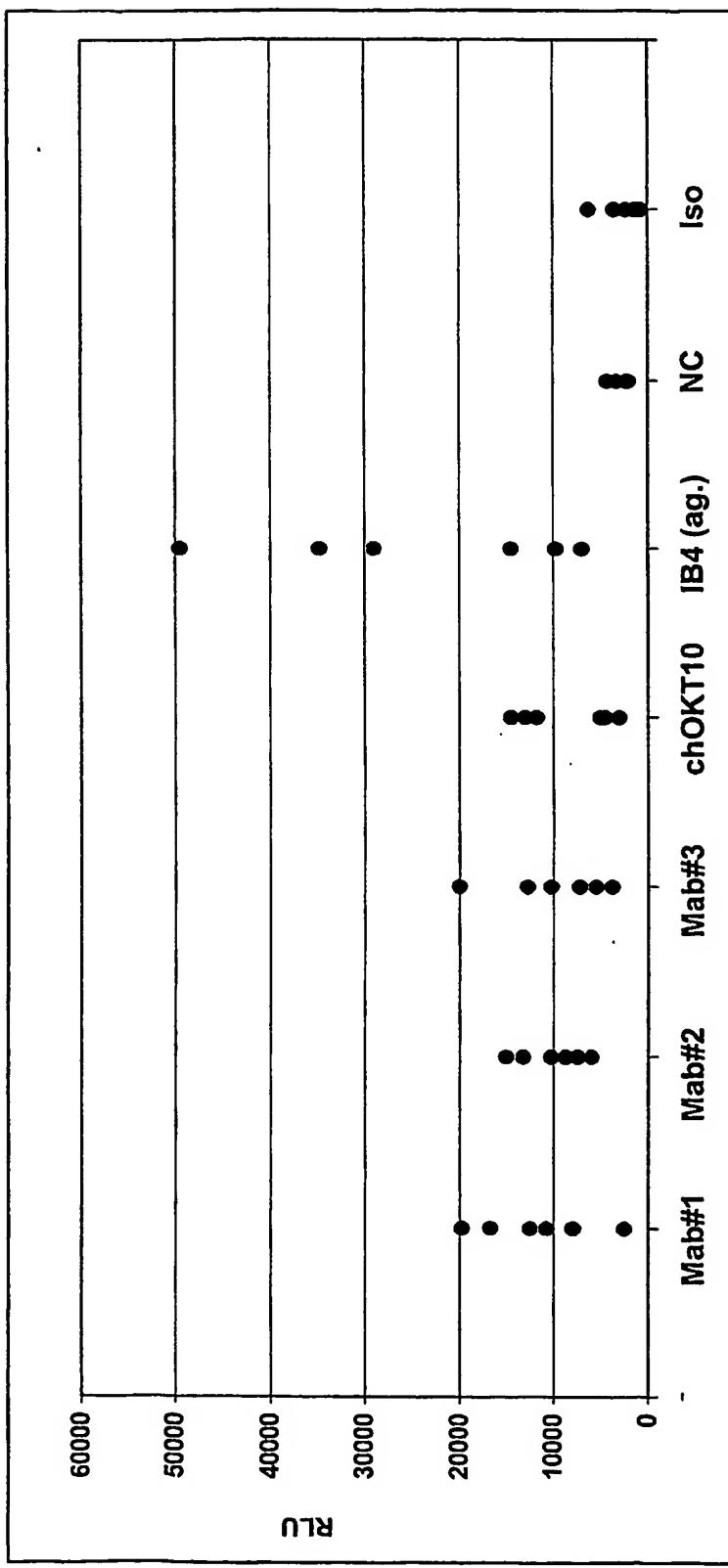


Fig. 12: IL-6 Release Assay

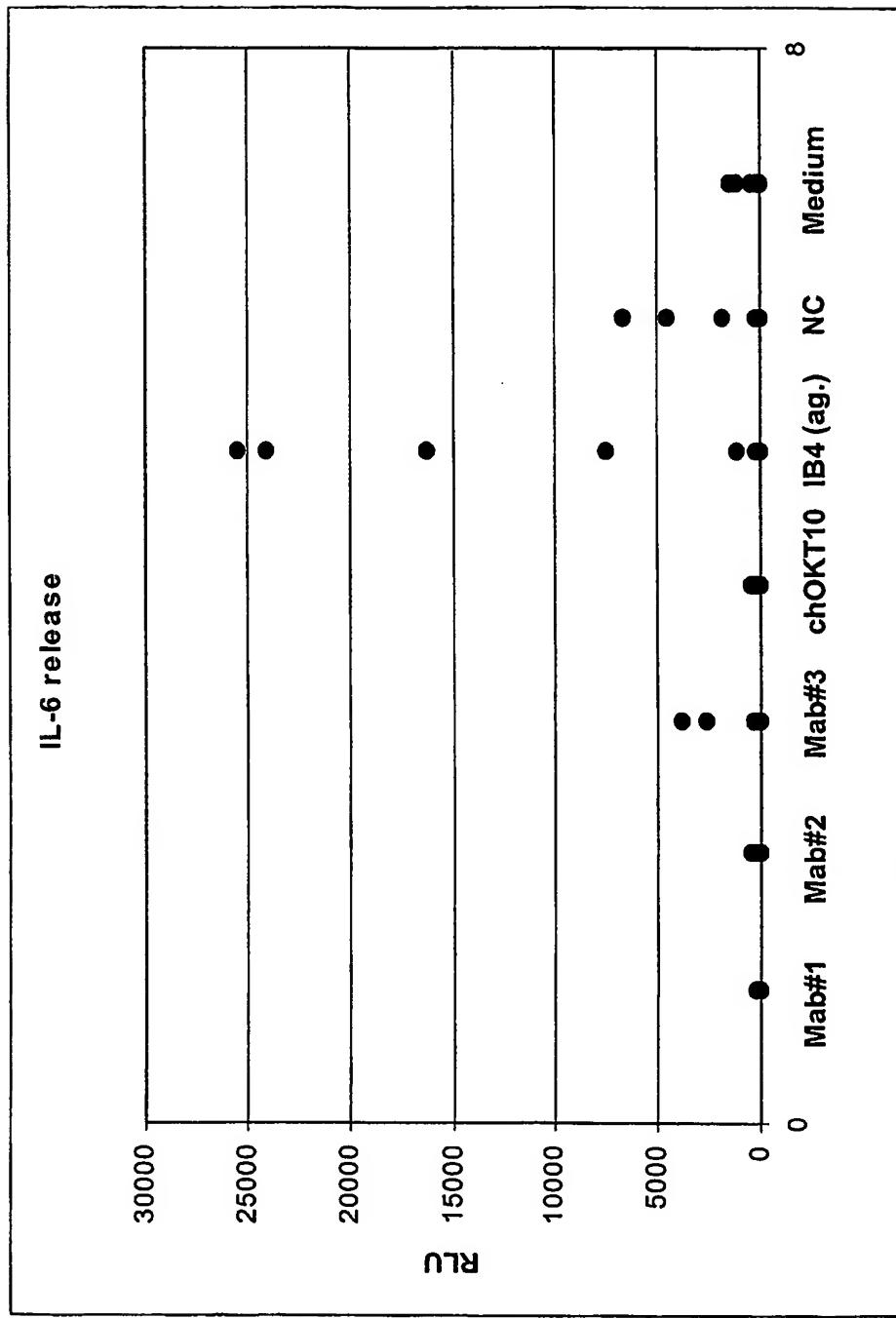


Fig. 13: Cytotoxicity towards CD34+/CD38+ progenitor cells

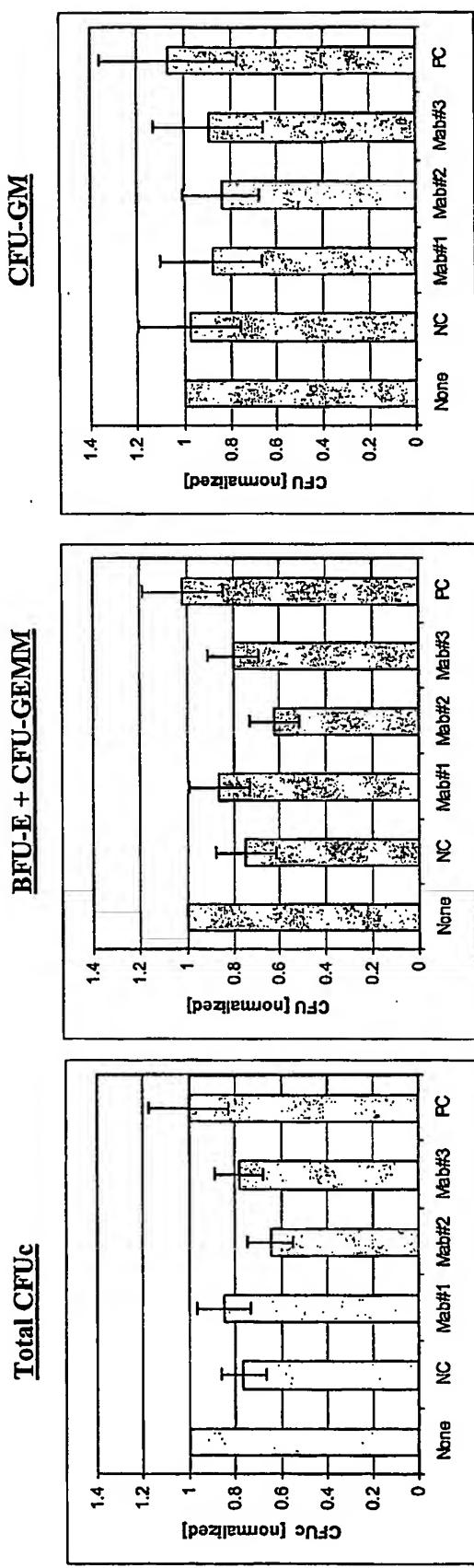


Fig. 14: ADCC with different cell-lines

Cell line	Culture Collection	Origin	Expression [MF1]	Max. specific killing [%] in ADCC ^{a,c}		
				Mab#1	Mab#2	Mab#3
RPMI 8226	ATCC CCL-155	MM	405.71	56	58	54
KMS-12-BM	DSMZ ACC551	MM	142.29	26	32	30
NCI-H929	ECACC95050415	MM	45.01	68	73	38
OPM-2	DSMZ ACC50	MM	37.99	6	13	3
U-266	ECACC85051003	MM	26.14	17	14	12
KMS-11	Namba et al., 1989 ^b	MM	26.81 ^d	22	30	26
JVM-13	DSMZACC19	CLL	463.93	11	20	12
JVM-2	DSMZACC12	CLL	140.84	22	28	10
CCRF-CEM	ECACC85112105	ALL	301.46	24	29	20
Jurkat	DSMZ ACC282	ALL	202.99	7	8	13
AML-193	DSMZ ACC549	AML	62.69 ^d	33	26	39
OCI-AML5	DSMZ ACC247	AML	207.55 ^d	20	21	16
NB-4	DSMZ ACC207	AML	164.7 ^d	36	38	32
THP-1	DSMZ ACC16	AML	34.41	64	59	38
HL-60 ^c	DSMZ ACC3	AML	18.43 ^a	29	35	29
Raji	Burkitt's Lymph.	Burkitt's lymph.	n.d.	53	62	48
						n.d.

Fig. 15: ADCC with MM-samples

Antibodies	Mab#1	Mab#2	Mab#3	PC
Parameters:				
MM samples: EC50 [nM] ^a :	0.116-0.202	0.006-0.185	0.027-0.249	0.282-0.356
MM samples: Max spec. killing [%]	13.1 - 61.6	16.2 - 57.9	13.6 - 36.0	15.5 - 49.5

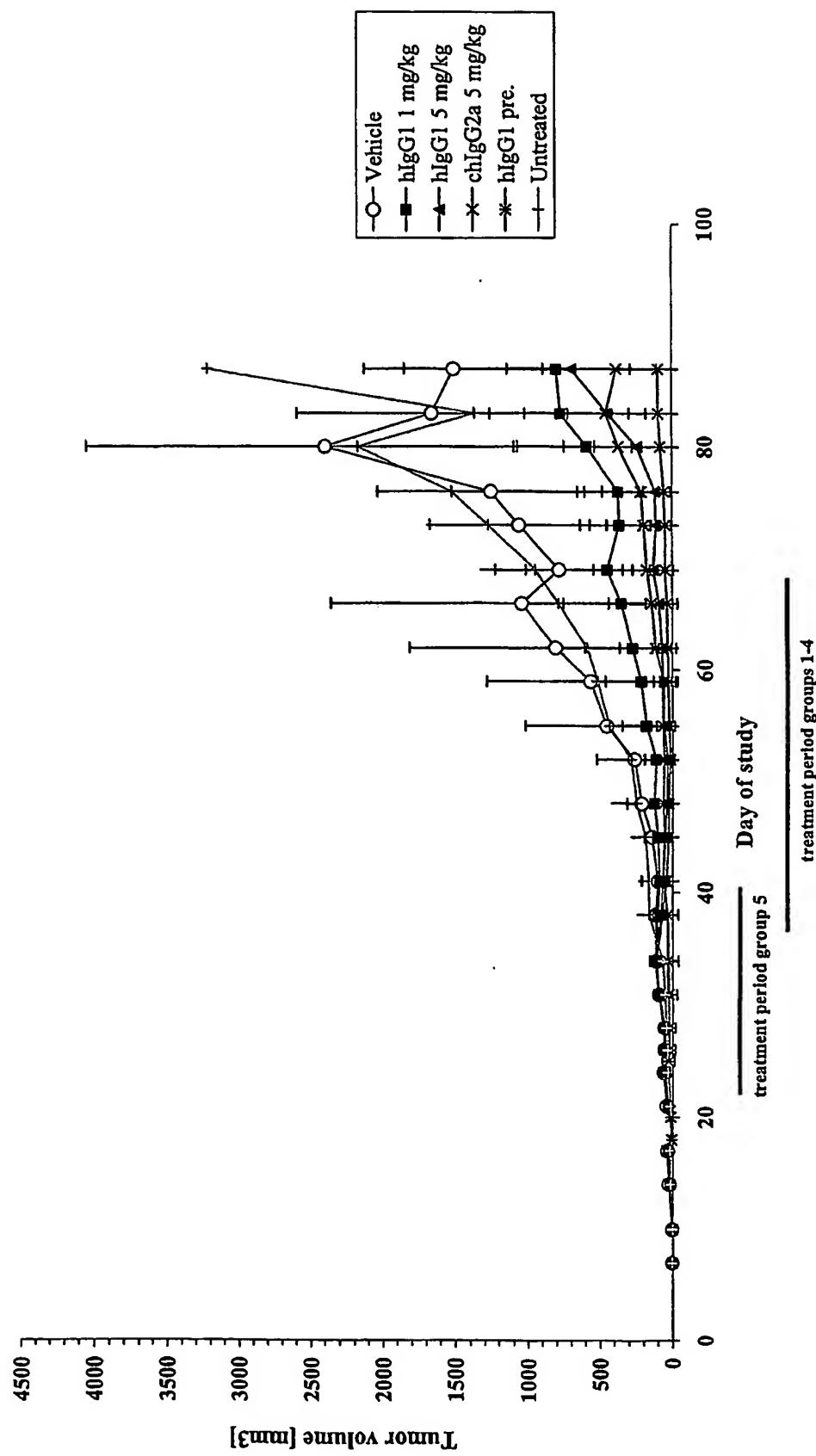


Fig. 16: Treatment of human myeloma xenograft with MOR03080